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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/852,472

DATE: 05/24/2001  
TIME: 13:17:23

**ENTERED**

Input Set : A:\97-28C1.SEQ.txt  
Output Set: C:\CRF3\05242001\I852472.raw

4 <110> APPLICANT: Sheppard, Paul O.  
5 Jelinek, Laura J.  
8 <120> TITLE OF INVENTION: Mammalian Neuro-Growth Factor Like  
9 Protein  
11 <130> FILE REFERENCE: 97-28C1  
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/852,472  
C--> 13 <141> CURRENT FILING DATE: 2001-05-10  
13 <150> PRIOR APPLICATION NUMBER: 09/099,295  
14 <151> PRIOR FILING DATE: 1998-06-18  
16 <150> PRIOR APPLICATION NUMBER: 60/050,143  
17 <151> PRIOR FILING DATE: 1997-06-18  
19 <160> NUMBER OF SEQ ID NOS: 24  
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 1297  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Homo sapiens  
28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (69)...(887)  
32 <400> SEQUENCE: 1  
33 aagcttggca cgaggtggca cgaggcctcg tgccaagctt ggcacgaggg cgccctggagg 60  
34 cacaggcc atg agg ggc tct cag gag gtg ctg atg tgg ctt ctg gtg 110  
35 Met Arg Gly Ser Gln Glu Val Leu Met Trp Leu Leu Val  
36 1 5 10  
38 ttg gca gtg ggc ggc aca gag cac gcc tac cgg ccc ggc cgt agg gtg 158  
39 Leu Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
40 15 20 25 30  
44 tgt gct gtc cgg gct cac ggg gat cct gtc tcc gag tgc ttc gtg cag 206  
45 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln  
46 35 40 45  
48 cgt gtg tac cag ccc ttc ctc acc acc tgc gac ggg cac cgg gcc tgc 254  
49 Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys  
50 50 55 60  
52 agc acc tac cga acc atc tat agg acc gcc tac cgc cgc agc cct ggg 302  
53 Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly  
54 65 70 75  
56 ctg gcc cct gcc agg cct cgc tac gcg tgc tgc ccc ggc tgg aag agg 350  
57 Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg  
58 80 85 90  
60 acc agc ggg ctt cct ggg gcc tgt gga gca gca ata tgc cag ccg cca 398  
61 Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro  
62 95 100 105 110  
64 tgc cgg aac gga ggg agc tgt gtc cag cct ggc cgc tgc cgc tgc cct 446  
65 Cys Arg Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro  
66 115 120 125  
68 gca gga tgg cgg ggt gac act tgc cag tca gat gtg gat gaa tgc agt 494

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69 Ala Gly Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser
70      130      135      140
72 gct agg agg ggc ggc tgt ccc cag cgc tgc gtc aac acc gcc ggc agt 542
73 Ala Arg Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser
74      145      150      155
76 tac tgg tgc cag tgt tgg gag ggg cac agc ctg tct gca gac ggt aca 590
77 Tyr Trp Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr
78      160      165      170
80 ctc tgt gtg ccc aag gga ggg ccc ccc agg gtg gcc ccc aac ccg aca 638
81 Leu Cys Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr
82 175      180      185
86 gga gtg gac agt gca atg aag gaa gaa gtg cag agg ctg cag tcc agg 686
87 Gly Val Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg
88      195      200      205
90 gtg gac ctg ctg gag gag aag ctg cag ctg gtg ctg gcc cca ctg cac 734
91 Val Asp Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His
92      210      215      220
94 agc ctg gcc tcg cag gca ctg gag cat ggg ctc ccg gac ccc ggc agc 782
95 Ser Leu Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser
96      225      230      235
98 ctc ctg gtg cac tcc ttc cag cag ctc ggc cgc atc gac tcc ctg agc 830
99 Leu Leu Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser
100      240      245      250
102 gag cag att tcc ttc ctg gag gag cag ctg ggg tcc tgc tcc tgc aag 878
103 Glu Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
104 255      260      265      270
106 aaa gac tcg tgactgccca gcgccccagg ctggactgag cccctcacgc 927
107 Lys Asp Ser
109 cgccctgcag ccccatgcc cctgcccac atgctggggg tccagaagcc acctcgggg 987
110 gactgagcgg aagccaggc agggccttc tcctcttct cctccccttc ctcaaggaggc 1047
111 tccccagacc ctggcatggg atgggctggg atcttctctg tgaatccacc cctggctacc 1107
112 cccaccctgg ctaccccaac ggcattccaa ggccaggtgg gccctcagct gaggaagg 1167
113 acgagctccc tgctggagcc tgggacccat ggcacaggcc aggcagccc gaggtgggt 1227
114 ggggcctcag tgggggctgc tgcctgacct ccagcacaat aaaaatgaaa cgtgaaaaaa 1287
115 aaaaaaaaaa 1297
117 <210> SEQ ID NO: 2
118 <211> LENGTH: 273
119 <212> TYPE: PRT
120 <213> ORGANISM: Homo sapiens
122 <400> SEQUENCE: 2
123 Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu Ala
124 1      5      10      15
127 Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala
128      20      25      30
129 Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
130      35      40      45
131 Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
132      50      55      60
133 Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala

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```

134 65                               70                               75                               80
135 Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser
136                               85                               90                               95
137 Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg
138                               100                               105                               110
139 Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly
140                               115                               120                               125
141 Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg
142                               130                               135                               140
143 Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
144 145                               150                               155                               160
145 Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
146                               165                               170                               175
147 Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val
148                               180                               185                               190
149 Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp
150                               195                               200                               205
151 Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu
152                               210                               215                               220
153 Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
154 225                               230                               235                               240
155 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln
156                               245                               250                               255
157 Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp
158                               260                               265                               270
159 Ser
161 <210> SEQ ID NO: 3
162 <211> LENGTH: 254
163 <212> TYPE: PRT
164 <213> ORGANISM: Homo sapiens
166 <400> SEQUENCE: 3
167 Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala Val Arg Ala
168 1                               5                               10                               15
169 His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val Tyr Gln Pro
170                               20                               25                               30
171 Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr Tyr Arg Thr
172                               35                               40                               45
173 Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala Pro Ala Arg
174                               50                               55                               60
175 Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser Gly Leu Pro
176 65                               70                               75                               80
177 Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly
178                               85                               90                               95
179 Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly
180                               100                               105                               110
181 Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly
182                               115                               120                               125
183 Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys
184                               130                               135                               140

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```

185 Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys
186 145 150 155 160
187 Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala
188 165 170 175
189 Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu Glu
190 180 185 190
191 Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala Ser Gln
192 195 200 205
193 Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu Val His Ser
194 210 215 220
195 Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln Ile Ser Phe
196 225 230 235 240
197 Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp Ser
198 245 250
200 <210> SEQ ID NO: 4
201 <211> LENGTH: 284
202 <212> TYPE: DNA
203 <213> ORGANISM: Homo sapiens
205 <400> SEQUENCE: 4
206 ggcggcgccg cgtgcgcgcc ccggatccgg cggccaccca gaggagaagg ccaccccgcc 60
207 tggaggcaca ggccatgagg ggctctcagg aggtgctgct gatgtggctt ctggtgttgg 120
208 cagtgggagg cacagagcac gcctaccggc ccggccgtag ggtgtgtgct gtccgggctc 180
211 acgggggacc tgtctccgag tcgttcgtgc agcgtgtgta ccagcccttc ctcaccacct 240
212 gcgacgggca ccgggcctgc agcacctacc gaaccatcta tagg 284
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 40
216 <212> TYPE: DNA
217 <213> ORGANISM: Homo sapiens
219 <400> SEQUENCE: 5
220 tgcggcggtg ggcggtccta tagatgggtc ggtaggtgct 40
222 <210> SEQ ID NO: 6
223 <211> LENGTH: 18
224 <212> TYPE: DNA
225 <213> ORGANISM: Homo sapiens
227 <400> SEQUENCE: 6
228 gctgatgtgg cttctggt
230 <210> SEQ ID NO: 7
231 <211> LENGTH: 18
232 <212> TYPE: DNA
233 <213> ORGANISM: Homo sapiens
235 <400> SEQUENCE: 7
236 ggtaggcgtg ctctgtgc 18
238 <210> SEQ ID NO: 8
239 <211> LENGTH: 708
240 <212> TYPE: PRT
241 <213> ORGANISM: Homo sapiens
243 <400> SEQUENCE: 8
244 Thr His Arg Gly Leu His Ile Ser Ala Leu Ala Thr Tyr Arg Ala Arg
245 1 5 10 15

```

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```

246 Gly Pro Arg Gly Leu Tyr Ala Arg Gly Ala Arg Gly Val Ala Leu Cys
247          20          25          30
250 Tyr Ser Ala Leu Ala Val Ala Leu Ala Arg Gly Ala Leu Ala His Ile
251          35          40          45
252 Ser Gly Leu Tyr Ala Ser Pro Arg Val Ala Leu Ser Glu Arg Gly
253          50          55          60
254 Leu Ser Glu Arg Pro His Glu Val Ala Leu Gly Leu Asn Ala Arg Gly
255 65          70          75          80
256 Val Ala Leu Thr Tyr Arg Gly Leu Asn Pro Arg Pro His Glu Leu Glu
257          85          90          95
258 Thr His Arg Thr His Arg Cys Tyr Ser Ala Ser Pro Gly Leu Tyr His
259          100         105         110
260 Ile Ser Ala Arg Gly Ala Leu Ala Cys Tyr Ser Ser Glu Arg Thr His
261          115         120         125
262 Arg Thr Tyr Arg Ala Arg Gly Thr His Arg Ile Leu Glu Thr Tyr Arg
263          130         135         140
264 Ala Arg Gly Thr His Arg Ala Leu Ala Thr Tyr Arg Ala Arg Gly Ala
265 145          150         155         160
266 Arg Gly Ser Glu Arg Pro Arg Gly Leu Tyr Leu Glu Ala Leu Ala Pro
267          165         170         175
268 Arg Ala Leu Ala Ala Arg Gly Pro Arg Ala Arg Gly Thr Tyr Arg Ala
269          180         185         190
270 Leu Ala Cys Tyr Ser Cys Tyr Ser Pro Arg Gly Leu Tyr Thr Arg Pro
271          195         200         205
272 Leu Tyr Ser Ala Arg Gly Thr His Arg Ser Glu Arg Gly Leu Tyr Leu
273          210         215         220
274 Glu Pro Arg Gly Leu Tyr Ala Leu Ala Cys Tyr Ser Gly Leu Tyr Ala
275 225          230         235         240
276 Leu Ala Ala Leu Ala Ile Leu Glu Cys Tyr Ser Gly Leu Asn Pro Arg
277          245         250         255
278 Pro Arg Cys Tyr Ser Ala Arg Gly Ala Ser Asn Gly Leu Tyr Gly Leu
279          260         265         270
280 Tyr Ser Glu Arg Cys Tyr Ser Val Ala Leu Gly Leu Asn Pro Arg Gly
281          275         280         285
282 Leu Tyr Ala Arg Gly Cys Tyr Ser Ala Arg Gly Cys Tyr Ser Pro Arg
283          290         295         300
284 Ala Leu Ala Gly Leu Tyr Thr Arg Pro Ala Arg Gly Gly Leu Tyr Ala
285 305          310         315         320
286 Ser Pro Thr His Arg Cys Tyr Ser Gly Leu Asn Ser Glu Arg Ala Ser
287          325         330         335
288 Pro Val Ala Leu Ala Ser Pro Gly Leu Cys Tyr Ser Ser Glu Arg Ala
289          340         345         350
292 Leu Ala Ala Arg Gly Ala Arg Gly Gly Leu Tyr Gly Leu Tyr Cys Tyr
293          355         360         365
294 Ser Pro Arg Gly Leu Asn Ala Arg Gly Cys Tyr Ser Val Ala Leu Ala
295          370         375         380
296 Ser Asn Thr His Arg Ala Leu Ala Gly Leu Tyr Ser Glu Arg Thr Tyr
297 385          390         395         400
298 Arg Thr Arg Pro Cys Tyr Ser Gly Leu Asn Cys Tyr Ser Thr Arg Pro

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VERIFICATION SUMMARY

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Input Set : A:\97-28C1.SEQ.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date